

SEQUENCE LISTING

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 <212> PRT
 <213> Homo sapiens

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Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
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Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
 35 40 45

Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
 50 55 60

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Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
 65 70 75 80

Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
 85 90 95

25

Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
 100 105 110

Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
 115 120 125

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Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
 130 135 140

35

Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
 145 150 155 160

Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
 165 170 175

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Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
 180 185 190

Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
 195 200 205

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Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
 210 215 220

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Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
 225 230 235 240

Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
 245 250 255

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Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
 260 265 270

Ser Ile Pro Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
 275 280 285

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Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
 290 295 300

65

Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
 305 310 315 320

Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
 325 330 335

Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
 340 345 350

5 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
 355 360 365

Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
 370 375 380

10 Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
 385 390 395 400

15 Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
 405 410 415

Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
 420 425 430

20 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
 435 440 445

Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
 450 455 460

25 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
 465 470 475 480

30 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
 485 490 495

Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
 500 505 510

35 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
 515 520 525

Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
 530 535 540

40 Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val
 545 550 555 560

Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser
 565 570 575

Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly
 580 585 590

50 Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly
 595 600 605

Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val
 610 615 620

55 Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr
 625 630 635 640

60 Ile Ile Leu Ile Tyr Ala Met Lys Lys Tyr Gln Glu Lys Asp Ile
 645 650 655

Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser
 660 665 670

65 Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu
 675 680 685

Thr His Cys

690

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 attttatcta tcgtacgttt cataacttt gaaataacaa aaagactaaa ctgtagagtt 240
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 atgaatagga aaaacatttg actcttacag acataattat agtgttaata tacacagttc 180
 gcccatttaac aacacaggtt taaactacgc gtttcaactt ctatgcaaat tttgtccatc 240
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 aatttgtaat agaaatgcta aaattaatgt taaaatgaa acactcttctt atctacatag 180
 30 gttgtttaaa ggaatctggg 200

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 taagcacaca tgcggaaaac atttttcaaa ataaactgaat tcactcttc aatagtcctt 120
 tgcttaatat aatttagaaag ttacaagtag gaaataaatg tattactaat cagaataaat 180
 ataaaatcca gtccttattt 200

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 cccctctt gtcctttct tctctctc tcttttgc atatgtctat catatattc 180
 55 cagaaataat ccagtgcacat ctc 203

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<400> 11
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 tataaaacaca cctaatgata tgcattttt tacataatactggaaattt caaattcata 120
 65 tttcatcaaa tttaatttt ctgagaattt attttattaa aatttactat gaactctcaa 180
 ggctgttaatt aataattttg c 201

100135

-6-

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ataaacgaat cctccaaatt tttgaactt tatttaatca aaatatatca atgtgaaata 120
tcatgcagtt acatttaaa tatgtccct aaactgacat cttctttct cctattacag 180
10 gaggattct agctccaata 200